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NiceProt View of TrEMBL: O48663

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General information about the entry

Entry name O48663
Primary accession number O48663
Secondary accession numbers None
Entered in TrEMBL in Release 06, June 1998
Sequence was last modified in Release 06, June 1998
Annotations were last modified in Release 22, October 2002
Name and origin of the protein
Protein name Chloroplast w6 desaturase
Synonyms None
Gene name DES6
From Chlamydomonas reinhardtii [TaxID: 3055]
Taxonomy Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

References

- 1) SEQUENCE FROM NUCLEIC ACID.
MEDLINE=98158334; PubMed=9498569; [NCBI, ExPASy, EBI, Israel, Japan]
Sato N., Fujiwara S., Kawaguchi A., Tsuzuki M.;
"Cloning of a gene for chloroplast w6 desaturase of a green alga, Chlamydomonas reinhardtii.";
J. Biochem. 122:1224-1232(1997).

Comments

None

Cross-references

EMBL AB007640; BAA23881.1; - [EMBL / GenBank / DDBJ] [CodingSequence]
InterPro IPR005804: FA_desat_fam.
Graphical view of domain structure.
Pfam PF00487: FA_desaturase_1.
ProDom PD001081: FA_desat_fam_2.
[Domain structure / List of seq. sharing at least 1 domain].
ProteinMap O48663.
PROSAGE O48663
ModBase O48663.
SWISS-2DPAGE GET REGION ON 2D PAGE.

Keywords

None

Features

None

Sequence information

Length: 424 AA Molecular weight: 48377 Da CRC64: D553054C1CEE6B0D [This is a checksum on the sequence]

10 20 30 40 50 60

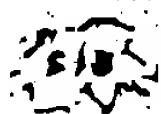
```

AFALRSPGA VRAPACAQRA SGVRAAKPGF LRSAAYARPQ VQTNAALSV PVNQLTOEER
      70      80      90      100      110      120
NLARELGKY SIGRELPONV SLTDIIKSMP AEYFKLDHGK AWRACLTIA ACSACWYLIS
      130      140      150      160      170      180
SPWYLLPAA WALAGTAFTG CFVIGHDCGH RSEHNNLIE DIVGHIFFAP LIYPFEPWRI
      190      200      210      220      230      240
HNHHHAHTN KLVEDTAWHP VTEADMAKWD STSAMLYKVF LGTPLKLWAS VGHVWVWHPD
      250      260      270      280      290      300
NKYTPKQRT RVVISLAVVY GFMTAFAPAL LYEGGPWAFV KYWLMPWLGY HFWMSTFTVY
      310      320      330      340      350      360
HTAPHIPFK KAEWNAAKA QLSGTVHCDF PNWVEFLTHD ISWHVPHHVA PKIPWYNLRK
      370      380      390      400      410      420
TESLRENWG QYMTECTFNW RVVKNICTEC HVDYKVNKY PFDYKKEEAL FAVQRRVLPD

```

cf SEQ ID no: 11.

AAF

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[EMBLnet-CH/SIB \(Switzerland\)](#)Direct BLAST submission at [NCBI \(Bethesda, USA\)](#)[ScanProsite](#), [MotifScan](#)

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[\[Tools\]](#)

General information about the entry

Entry name O53604
Primary accession number O53604
Secondary accession numbers None
Entered in TrEMBL in Release 06, June 1998
Sequence was last modified in Release 06, June 1998
Annotations were last modified in Release 20, March 2002
Name and origin of the protein
Protein name Hypothetical protein Rv0059
Synonyms None
Gene name RV0059 or MTV030.02 or MT0065
From *Mycobacterium tuberculosis* [TaxID: 1773]
Taxonomy *Bacteria*; *Actinobacteria*; *Actinobacteridae*; *Actinomycetales*;
Corynebacterineae; *Mycobacteriaceae*; *Mycobacterium*.

References

- 1) SEQUENCE FROM NUCLEIC ACID.
STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230; [NCBI, ExPASy, EBI, Israel, Japan]
Colt S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltywell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLaren L., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrall B.G.
"Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence."; *Nature* 393:537-544(1998).
- 2) SEQUENCE FROM NUCLEIC ACID.
STRAIN=CDC 1551 / Oshkosh;
Flaeschmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Enomoto M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khoui H., Gill J., Mikula A., Bishai W.
"Whole genome comparison of *Mycobacterium tuberculosis* clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

Comments

None

Cross-references

EMBL AL021428; CAA16240.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
AF006919; AAK44287.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
FGR MT0065; -.
TubercuList Rv0059; -.
ProDom [Domain structure / List of seq. sharing at least 1 domain].
ProtoMap O53604.

RESAGE O53604.
IodBase O53604.
WISS-2DPAGE GET REGION ON 2D PAGE
Keywords

hypothetical protein; Complete proteome.

Features

One

Sequence information

Length: 230 AA Molecular weight: 25580 Da CRC64: 1A109D34B16590A8 [This is a checksum on the sequence]

10 20 30 40 50 60
ITRYKPESG FVARSGGPDR KRPHDWTVMH FTHADNLPGI ITAGRLLADS AVTPTTEVAY
70 80 90 100 110 120
PVKELRRHK WAPDSRYPA SMASDHVPFY IAARSPMLYV VCKGHSGYSG GAGPLVHLGV
130 140 150 160 170 180
LGDIIDADL TWCASDGNAAS YTKFSRQV DTLGTFVDFD LLCQRQWHNT DDDPNRQSRR
190 200 210 220 230
AEILVYGHV PFELVSYVCC YNTETMTRVR TLLDPVGGVR KYVIKPGMY

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Direct BLAST submission at NCBI (Berthesda, USA)



ScanProsite, MotifScan



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)



Feature table viewer (Java)



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